

FIGURE 1 (1/2)

	1		50
{CAA69226}	MQIPRAALLP	LLLLLLAAPA	SAQLSRAGRS
{PRSS11-Like}	~~~~~	~~~~~	~~~~~
{AAB94569}	~~~~~	~~~~~	~MAAPRAGRG
Consensus	-----	-----	-----
	51		100
{CAA69226}	EHCEGGRARD	ACGCCEVCGA	PEGAACGLQE
{PRSS11-Like}	~~~~~	~~~~~	~~~~~
{AAB94569}	RLTPDLRALL	TSGTSD...P	RARVTYGTPS
Consensus	-----	-----	-----
	101		150
{CAA69226}	VRRRAQAGLC	VCASSEPVCG	SDANTYANLC
{PRSS11-Like}	~~~~~	~~~~~	~~~~~
{AAB94569}	PGPRAQLTAV	TPDTRTREAS	ENSGTRSRAW
Consensus	-----	-----	-----
	151		200
{CAA69226}	QRGACGQGE	D..PNSLRHK	YNFIADVVEK
{PRSS11-Like}	ALPA.SAGLH	Q..LSSPRYK	FNFIADVVEK
{AAB94569}	GPPAVLAAMP	SPPPASPRSQ	YNFIADVVEK
Consensus	---A-----	-----S-R--	-NFIADVVEK
	201	*	250
{CAA69226}	VPVASGSGFI	VSEDGLIVTN	AHVVTN....
{PRSS11-Like}	VPLSSGSGFI	MSEAGLIITN	AHVSSNSAA
{AAB94569}	VPISNGSGFV	VAADGLIVTN	AHVVD....
Consensus	VP---GSGF-	----GLI-TN	AHVV-----

FIGURE 1 (1/2)

	251	*		300
{CAA69226}	KDVDEKADIA	LIKIDHQGKL	PVLLLGSRSE	LRPGEFVVAI GSPFSLQNTV
{PRSS11-Like}	KDIDKKS DIA	TIKIHPKKKL	PVLLLGHSAD	LRPGEFVVAI GSPFALQNTV
{AAB94569}	TAVDPVADIA	TLRIQTKEPL	PTLPLGRSAD	VRQGEFVVAM GSPFALQNTI
Consensus	---D---DIA	---I-----L	P-L-LG-S--	-R-GEFVVA- GSPF-LQNT-
	301		*	350
{CAA69226}	TTGIVSTTQR	GGKELGLRNS	DMDYIQTDAI	INYGNSSGGPL VNLDGEVIGI
{PRSS11-Like}	TTGIVSTAQR	EGRELGLRDS	DMDYIQTDAI	INYGNSSGGPL VNLDGEVIGI
{AAB94569}	TSGIVSSAQR	PARDLGLPQT	NVEYIQTDAI	IDFGNSSGGPL VNLDGEVIGV
Consensus	T-GIVS--QR	----LGL---	---YIQTDA-	I--GNSGGPL VNLDGEVIG-
	351			400
{CAA69226}	NTLKVTAGIS	FAIPSDKIKK	FLTESHDR.Q	AKGKAITKKK YIGIRMMSLT
{PRSS11-Like}	NTLKVTAGIS	FAIPSDRITR	FLTEFQDK.Q	IKD...WKKR FIGIRMRTIT
{AAB94569}	NTMKVTAGIS	FAIPSDRLRE	FLHRGEKKNS	SSGISGSQRR YIGVMMLTLS
Consensus	NT-KVTAGIS	FAIPSD----	FL-----	----- -IG--M----
	401			450
{CAA69226}	SSKAKELKDR	HRDFPDVISG	AYIIEVIPDT	PAEAGGLKEN DVIISINGQS
{PRSS11-Like}	PSLVDELKAS	NPDFPEVSSG	IYVQEVAPNS	PSQRGGIQDG DIIVKVNGRP
{AAB94569}	PSILAEQLR	EPSFPDVQHG	VLIHKVILGS	PAHRAGLRPG DVILAIGEOM
Consensus	-S---EL---	---FP-V--G	-----V----	P----G---- D-I-----
	451			489
{CAA69226}	VVSANDVSDV	IKRESTLNMV	VRRGNEDIMI	TVIPEEIDP
{PRSS11-Like}	LVDSSSELQEA	VLTESPLLE	VRRGNDDLLE	SIAPEVVM~
{AAB94569}	VQNAEDVYEA	VRTQSQLAVQ	IRRGRETTLT	YVTPEVTE~
Consensus	-----	----S-L---	-RRG-----	---PE----

FIGURE 2 (1/1)

HtrA3 (BC034390) x PRSS11-Like (SEQ ID No:2):

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101 CALQAASRRALQLSGTPVRQLQKGACP..LGLHQLSSPRYKFNFIADVVE 148
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
1   .....MHLALPASAGLHQLSSPRYKFNFIADVVE 29

149 KIAPAVVHIELFLRHPLFGRNVPLSSGSGFIMSEAGLIITNAHVSSNSA 198
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
30  KIAPAVVHIELFLRHPLFGRNVPLSSGSGFIMSEAGLIITNAHVSSNSA 79

199 APGRQQLKVQLQNGDSYEATIKDIDKKSDIATIKIHPKKKL PVL LLGHSA 248
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
80  APGRQQLKVQLQNGDSYEATIKDIDKKSDIATIKIHPKKKL PVL LLGHSA 129

249 DLRPGEFVVAIGSPFALQNTVTTGIVSTAQREGRELGLRDSMDYIQTDA 298
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
130 DLRPGEFVVAIGSPFALQNTVTTGIVSTAQREGRELGLRDSMDYIQTDA 179

299 IINYGNSSGGPLVNLDGEVIGINTLKV TAGISFAIPSDRITRFLTEFQDKQ 348
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
180 IINYGNSSGGPLVNLDGEVIGINTLKV TAGISFAIPSDRITRFLTEFQDKQ 229

349 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVAPNSPSQ 398
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
230 IKDWKKRFIGIRMRTITPSLVDELKASNPDFPEVSSGIYVQEVAPNSPSQ 279

399 RGGIQDGDIIIVKVNGRPLVDSSSELQEAVLTESPL LLEVRRGNDDLLFSIA 448
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
280 RGGIQDGDIIIVKVNGRPLVDSSSELQEAVLTESPL LLEVRRGNDDLLFSIA 329

449 PEVVM 453
      | | | |
330 PEVVM 334

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FIGURE 3 (1/1)

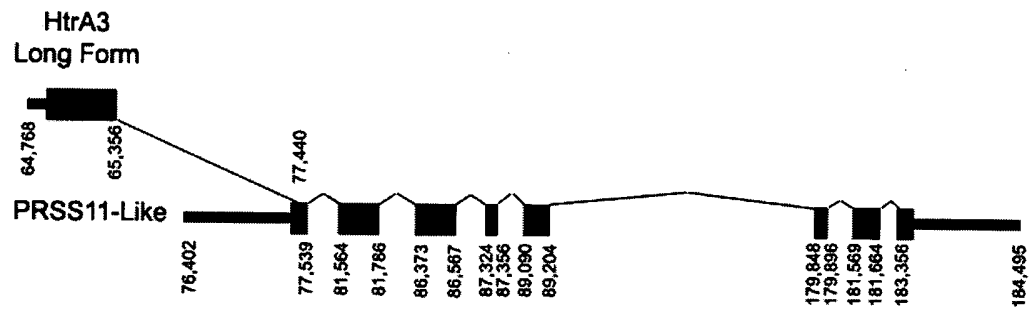


FIGURE 4

A. Unique HtrA3 Long Form Exons

E1 589-bp 12,083-bp E2
GCGCCTGCCCGTTGG**gt**aagcgctcgggg... ..ttcccgccagcg**ag**GTCTCCACCAGCTGA

E2 100-bp 4,024-bp E3
AGAGCTCTTCCTGAG**gt**gggtgaatacccc... ..tctccctggctg**ag**ACACCCGCTGTTTGG

B. Unique PRSS11-Like Exon

E1 1,138-bp 4,024-bp E2
AGAGCTCTTCCTGAG**gt**gggtgaatacccc... ..tctccctggctg**ag**ACACCCGCTGTTTGG

C. Common HtrA3 Long form and PRSS11-Like Exons

E3/E2 223-bp 4,586-bp E4/E3
AAGATCCATCCCAAG**gt**gggtgggctggg... ..ccttctctctcct**ag**AAAAAGCTCCCTGTG

E4/E3 195-bp 756-bp E5/E4
GATGCCATCATCAAC**gt**gagtgccaggac... ..ttcctccccttg**ag**TACGGGAAGTCCGGG

E5/E4 33-bp 1,733-bp E6/E5
CCACTGGTGAACCTG**gt**aagtgtcccctag... ..tacctccctgccc**ag**GATGGCGAGGTCATT

E6/E5 115-bp 90,643-bp E7/E6
ACAAGCAGATCAAAG**gt**aaagagctcacct... ..gtgtttcatttcc**ag**ACTGGAAGAAGCGCT

E7/E6 49-bp 1,672-bp E8/E7
GACGATCACACCAAG**gt**gagtggtctgaaga... ..gcagactctttcc**ag**CCTGGTGGATGAGCT

E8/E7 96-bp 1,691-bp E9/E8 1140-bp
TTCACCTTCTCAGAG**gt**taggctctgccaga... ..ctctcctgttggc**ag**AGGCGGCATCCAAGA